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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 ,
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1097
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         FGFI MOUSE
FGFI MOUSE
FGFB CHICK
FGFB HUMAN
FGFB HUMAN
FGFF HUMAN
FGF7 MOUSE
FGF7 SHEEP
FGF7 SHEEP
FGF7 PIG
FGF7 PIG
FGF7 LUMAN
FGF9 HUMAN
FGF9 HUMAN
FGF9 HUMAN
FGF9 RAT
FGF1 MOUSE
FGF1 MESAU
FGF1 MESAU
FGF1 HUMAN
FGF2 CHICK
FGF2 CHICK
FGF2 CHICK
FGF6 RAT
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  FGFA_XENLA
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089101 mus musculu
088182 rattus norv
090722 gallus gall
060258 homo sapien
070627 mus musculu
P55075 homo sapien
p37237 mus musculu
P21781 homo sapien
p36363 mus musculu
P48808 ovis aries
P79150 canis famil
011184 caenorhabdi
090198 sus scrofa
 P48800
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1 rattus norv
10 mus musculu
10 homo sapien
11 homo sapien
12 sus scrofa
2 sus scrofa
2 sus scrofa
2 senopus lae
homo sapien

xenopus lae
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homo sapien
homo sapien
bos taurus
gallus gallus gallus gallus gallus gall
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45	44	43	42	41	40	39	38	37	36	35	34
151.5	152	153	154	154	154.5	156.5	156.5	157	157.5	157.5	159
13.8	13.9	13.9	14.0	14.0	14.1	14.3	14.3	14.3	14.4	14.4	14.5
154	245	245	237	220	155	207	202	208	155	155	215
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FGF2_MOUSE	FGFD_HUMAN	FGFD_MOUSE	FGF3_XENLA	FGF3_CHICK	FGF1_CHICK	FGFG_HUMAN	FGF4_MOUSE	FGF6_HUMAN	FGF2_SHEEP	FGF2_BOVIN	FGFA_RAT
	Q92913 homo sapien										

## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; AF075292; AAC62240.1; EMBL; AF07422; BAA31986.1; EMBL; AF211188; AAF22977.1;	SEQUENCE FROM N.A.  Deisher T., Conklin D., Raymond F., Bukowski T., Holderman S.,  Hansen B., Sheppard P., O'Hara P.;  "Homo sapiens homologue of fibroblast growth factor.";  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  [4]  SEQUENCE FROM N.A.  TISSUE-Ovary;  Strausberg R.;  SUBMITTER (APR-2001) to the EMBL/GenBank/DDBJ databases.  -!- FUNCTION: STIMULATES HEPATIC AND INTESTINAL PROLIFERATION.  -!- SUBCELULAR LOCATION: Secreted (By similarity).  -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE-98414622; PubMed=9742123; Hu M.CT., Qiu W.R., Wang YP., Hill D., Ring B.D., Scully S., Hu M.CT., Qiu W.R., Wang YP., Hill D., Ring B.D., Scully S., Bolon B., Derose M., Luethy R., Simonet W.S., Arakawa T., Danilenko D.M.; "FGF-18, a novel member of the fibroblast growth factor family, stimulates hepatic and intestinal proliferation."; Mol. Cell. Biol. 18:6063-6074(1998). [2] SEQUENCE FROM N.A. TISSUE-Lung; MEDLINE-98325019; PubMed-9660775; Ohbayashi N., Hoshikawa M., Kimura S., Yamasaki M., Fukui S., Ito N.; "Structure and expression of the mRNA encoding a novel fibroblast growth factor, FGF-18."; J. Biol. Chem. 273:18161-18164(1998).	RESULT 1  FGFI_HUMAN  FGFI_HUMAN  STANDARD; PRT; 207 AA.  O76093;  AC 076093;  DT 15-JUL-1999 (Rel. 38, Created)  DT 15-JUL-1999 (Rel. 38, Last sequence update)  DT 15-JUN-2002 (Rel. 41, Last annotation update)  DT Fibroblast growth factor-18 precursor (FGF-18) (zFGF5).  DE Fibroblast growth factor-18 precursor (FGF-18) (zFGF5).  GN FGF18.  GN FGF18.  CS Homo sapiens (Human).  CC Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  ON NOBI_TaxID-9606;

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RESULT 2
FGFI_MOUSE
ID FGFI_M
AC 089101
DT 15-JUL
NCBL_T
RN (1]
RP SEQUEN
RA HUM.(C
RA BOLON
RA HOLL
RT STIMUL
RT STIMUL
RT STIMUL
RT STIMUL
RT JESUI
RA ONDAY
RT STIW
RT GFF-J
RT STIW
RT STIW
RT JESUI
RA ONDAY
RT GTOWT!
RL J. B1(
RN SEQUEN
RA DEISH
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InterPro; IPR002348; IL1_HBGF.
InterPro; IPR002348; IL1_HBGF.
Pfam; pF00167; FGF; 1.
PPRODOM; PD000831, HB/F_growthfact; 1
R SMART; SM00442; FGF; 1.
R PROSITE; PS00247; HBGF_FGF; 1.
R PROSITE; PS00247; HBGF_FGF; 1.
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Best Local
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                                                                                                                                                                                                                                          Danilenko D.M.;
Parilenko D.M.;
FGF-18, a novel member of the fibroblast growth factor stimulates hepatic and intestinal proliferation.";
Mol. Cell. Biol. 18:6063-6074(1998).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98414622; PubMed=9742123;
Hu M.C.-T., Qiu W.R., Wang Y.-P., Hill D.,
Bolon B., Derose M., Luethy R., Simonet W.
                                                                                "Structure and expression of the mRNA growth factor, FGF-18.";
J. Biol. Chem. 273:18161-18164(1998).
                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-18 precursor (FGF-18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFI_MOUSE 089101;
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CARBOHYD
      Hansen
                                                                                                                                                     Ohbayashi N., Hoshikawa M., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                              SEQUENCE FROM N.A.
                                                                                                                                                                       MEDLINE=98325019; PubMed=9660775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:
MIM; 603726;
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      В.,
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    , Conklin
Sheppard
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28
39
137
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O'Hara P
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                      Bukowski
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vel fibroblast
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RESULT 3
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Best Local Sim
Matches 204;
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PRODOM; PRO00831; HB/F-growthfact; 1.
SMART; SM00442; FGF; 1.
SMO0442; FGF; 1.
Growth factor; Signal; Glycoprotein.
SIGNAL 1 27 POTENTIAL
CHAIN 28 207 POTENTIAL
CHAIN 39 39 N-LINKED
CARBOHYD 137 137 N-LINKED
SEQUENCE 207 AA; 23920 MW; CD5F987
                                                                                                                                                                                    FGFI_RAT STAN

O88182;

15-JUL-1999 (Rel. 3

15-JUL-1999 (Rel. 3

16-OCT-2001 (Rel. 4
                        STRAIN-Wistar; TISSUE-Embryo;
MEDLINE-98325019; PubMed-9660775;
Ohbayashi N., Hoshikawa M., Kimur
                                                                                              Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         Fibroblast
                                                                    SEQUENCE FROM N.A.
                                                                                                                                            Rattus norvegicus
                                                                                                                                                             FGF18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1277980; Fgf18.
InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
DBTMMC: PROOFF
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"Structure and growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF075291; AAC62239.1; -. EMBL; AB004639; BAA31980.1; -. EMBL; AF211187; AAF22976.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATES HEPATIC AND INTESTINAL PROLIFERATION.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P31371; 1G82
                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYSAPSACTCLCLHFLLLCFQVQVLVAEENVDFRIHVENQTRARDDVSRKQLRLYQLYSR
                                                                                                                                                                                                                                                                                                                                       GQPELQKPFKYTTVTKRSRRIRPTHP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGKHIQVLGRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKP 120
                                                                                                                                                                                                                                                                                                                           GQAELQKPFKYTTVTKRSRRIRPTHP
                                                                                                                                                                                                                                                                                                                                                                                                 DGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYSAPSACTCLCLHFLLLCFQVQVLAAEENVDFRIHVENQTRARDDVSRKQLRLYQLYSR
                                                                                                                                                                                                                                                                                                                                                                                  DGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                        growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
expression of the mRNA encoding FGF-18.";
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                        38, Created)
38, Last sequence update)
40, Last annotation updat
factor-18 precursor (FGF-
                                                                                                                                              (Rat)
                                                                                                                 Rodentia;
                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.5%;
99.0%;
                           Kimura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBROBLAST GROWTH FACTOR-18.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CD5F987B271628B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1081;
Pred. No. 1
                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                 207
                                                                                                                                                                         update)
(FGF-18).
                           Yamasaki M., Fukui S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-94
                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
            a novel fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 4
FGF8_C1CK
ID FGF8_C
AC Q90722
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 61-NOV
DE F1EDOD
GN FGF8.
OS Gallus
OC Eukary
OC Archos
OC Gallus
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Best Local
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Q90722;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
Fibroblast growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   SEQUENCE FROM N.A.
                          NCBI_TaxID=9031;
                                                  Archosauria; Aves;
                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                181
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SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                           GQPELQKPFKYTTVTKRSRRIRPTHP
                                                                                                                                                                                                                                                                                                                                                                             GQTELQKPFKYTTVTKRSRRIRPTHP
                                                                                                                                                                                                                                                                             DGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPK
                                                                                                                                                                                                                                                                                          DGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPK
                                                                                                                                                                                                                                                                                                                              TSGKHIQVLGRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKP
                                                                                                                                                                                                                                                                                                                                            TSGKHIQVLGRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00167; FGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB004638;
P31371; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor; Signal; Glycoprotein.

1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
28
39
39
137
207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                            (Chicken)
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAA31979.1; -.
                                                                                               35, Created)
35, Last sequence update)
35, Last annotation updat
factor-8 precursor (FGF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 F
39 N
137 N
: 23950 MW;
                                                  Neognathae;
                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBROBLAST GROWTH FACTOR-18.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1081; DB 1; Pred. No. 1.3e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D90EDD7B271628B8 CRC64;
                                                  Galliformes; Phasianidae;
                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                   n update)
(FGF-8)
                                                                                                                                                                214
                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                   (HBGF-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       207;
                                                  Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 5
FGFH_HUMAN
ID FGFH_S
AC 060258
AC 060258
DT 15-JUL
DT 15-JUL
DT 15-JUN
DE FIDTOD
GN FGF17.
OS HOMO S
OC EUKARY
OC MAMMAN
IN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA HOShik
RA FUKUI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
MEDLINE-98183421; PubMed-
Hoshikawa M., Ohbayashi N
Fukui S., Itoh N
                                                                                                                                        15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
Fibroblast growth f
FGF17.
                                                                                                                                                                                                         FGFH_HUMAN
O60258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                            SEQUENCE FROM N.A
                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U55189; AAB06713.1; -. HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vertebrate limb.";
Development 122:1737-1750(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogel A., Rodriguez C., Izpisua-Belmonte J.C.; "Involvement of FGF-8 in initiation, outgrowth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96232288; PubMed=8674413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=White leghorn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002209; HB/F_growthfact.
                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LHFLLLCFQVQVLVAEENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVL-GR 71
                                                                                      17.
17.
no sapiens (Human).
no sapiens (Human).
Netazoa; Chordata; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                            EFLNYPFNRRSKRTR
                                                                                                                                                                                                                                                                                                              PFKYTTVTKRSRRIR 202
                                                                                                                                                                                                                                                                                                                                         IVLENNYTALQNAKYEGWYMAFTRKGRPRKGSKTRQHQREVHFMKRLPKGHQTTEPHRRF
                                                                                                                                                                                                                                                                                                                                                       KVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKG----QPELQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                MHLFVLCLQAQVTV-QSPPNFTQHVREQSLVTDQLSRRLVRTYQLYSRTSGKHVQILDNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD000831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                  38, Created)
38, Last sequence update)
41, Last annotation updat
factor-17 precursor (FGF-
                                  PubMed=9514906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 F
31 N
137 N
207 N
207 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.3%;
56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN INITIATION, OUTGROWTH AND PATTERNING
                    N .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                       Yonamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
N-BESFA3CD13A2BC34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 574; DB 1;
Pred. No. 6.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
FIBROBLAST GROWTH FACTOR-8.
                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                     update)
(FGF-17).
                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                      A
                     Konishi
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                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                       Ozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
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DT 15
DT 15
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Best Local s
Matches 112
FGFH_MOUSE
070627;
15-JUL-1999
15-JUL-1999
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C. Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE A SIGNALING MOLECULE IN THE INDUCTION A
                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; HB/F_growthfact;
SMARF; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure and expression of a novel fibroblast growth factor, FGF-17, preferentially expressed in the embryonic brain."; Biochem. Biophys. Res. Commun. 244:187-191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB009249; EMBL; AF497475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002209;
InterPro; IPR002348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
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                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                    11 LCLHFLLLCFQVQVLVAEEN----VDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: DETECTED IN EMBRYOS AT E14.5, BUT NOT AT E10.5 AND E19.5. PREFERENTIALLY EXPRESSED IN THE NEUROEPITHELIA OF THE ISTHMUS AND SEPTUM OF THE EMBRYONIC BRAIN AT E14.5.
SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATTERNING OF THE EMBRYONIC BRAIN. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               w; HGNC:3673; FGF17.
603725; -.
                                                                                                                                        HAEKOKOFEFVGSAPTRRTKRTRRPQP 214
                                                                                                                                                                                                                                                                           VLGRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKPDGTSKEC
                                                                                                                                                                    -PELOKPEKY-----TTVTKRSRRIRP 203
                                                                                                                                                                                                 VFTEIVLENNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPN
                                                                                                                                                                                                                             VFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQ-----
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216
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IL1_HBGF.
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Pred. No. 1.3e-46;
8; Mismatches 39;
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N-LINKED (GLCNAC. . .) (POT
; 2EE0288675220F4C CRC64;
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P.D.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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ProDom; PD000831; HB/F_growthfact;
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 244:187-191(1998) -:- FUNCTION: MAY BE A SIGNALING MOLECULE IN THE PATTERNING OF THE EMBRYONIC BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and expression of a novel fibroblast growth preferentially expressed in the embryonic brain."; Biochem. Biophys. Res. Commun. 244:187-191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wistar; TISSUE=Embryo; MEDLINE=98183421; PubMed=9514906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoshikawa M.,
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188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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DEVELOPMENTAL STAGE: IN RAT, EXPRESSED EMBRYO AT E14.5. EXPRESSED AT LOWER LEV E10.5 AND E19.5.
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TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC BRAIN,
                                                                                                                                                                                                                      HAERQKQFEFVGSAPTRRTKRTRR
                                                                                                                                                                                                 VTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDC
                                                                                                                                                                                                                                                                                                 LCTOLLILCCOTO - - -
                                            -PELQKPFKY----TTVTKRSRR
                                                                                                VFTEIVLENNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPN
                                                                                                                                             VFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQ-----
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137
216 AA;
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a; Chordata;
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Pred. No. 3
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; 2EE94BDF75220F4C CRC64;
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FIBROBLAST GROWTH FACTOR-17
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.7e-46;
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EMBRYO AT
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FGF8_HUMAN
FGF8_HUMAN
AC P55075
DT FGF8_H
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DT 01-OCT
DT 16-OCT
CC Mammal
CO MACDLIT
CO MACDLIT
CO TANA
CO TAN
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                                                                                                                                                                                                                                                                                                                                                                                                       Ghosh A.K., &
                                                                                                                                                                                                                                        the European Bioinformatics Institute. use by non-profit institutions as lo modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96299767; PubMed-8661131; Gemel J., Gorry M., Ehrlich G.D., Macarthur C. "Structure and sequence of human FGF8."; Genomics 35:253-257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human
cells:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGF8_HUMAN STANDARD; PRT; 233 AA.
P55075; Q14915; Q15766;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Androgen-Induced growth factor precursor (AIGF) (HBGF-8) (Fibroblast growth factor-8) (FGF-8).
                                                                                                                                                                                                   entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Payson R.A., Wu J., Liu Submitted (JAN-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Prostate;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Payson R.A., Wu J., Liu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett.
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MEDLINE=95255551; PubMed=7737407;
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SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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U46212;
U46211;
$78466;
$78462;
$78463;
$78464;
$78465;
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                                                                                                                                                                                                   email to license@isb-sib.ch).
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AAB40955.1;
AAB40954.1;
AAB40953.1;
AAB34255.1;
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EMBL/GenBank/DDBJ databases.
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Best Local S
Matches 111
                                                                     8_MOUSE
FGF8_MOUSE
P37237;
01-OCT-1994
01-OCT-1994
                                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Androgen-induced growth factor precursor (AIG growth factor-8) (FGF-8).
                                                                                                                                                                                                                                                                                                                                                VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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EMBL;
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EMBL;
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                                  FGF8 OR AIGF.
                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor; Mitogen; Alternative splicing; Signal SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000831; HB
SMART; SM00442; FGF;
PROSITE; PS00247; HB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:3686; FGF8.
MIM; 600483; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U56978; AAB03787.1; HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002209; HB/F_growthfact
                                                                                                                                                181
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                                                                                                                                                                                     121
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hes 111;
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                                                                                                                                                                                                                                                                               1 MYSAPSACTCLCLHFLLLCFQVQ------VLVAEENVDFRI------HVENQTRA 43
                                                                                                                                                                                                                        SKTRQHQREVHFMKRLPRGHHTTEQSLRF
                                                                                                                                                           PKTRENQQDVHFMKRYPKGQPELQKPFKY
                                                                                                                                                                                    ETGLYICMNKKGKLIAKSNGKGKDCVFTEIVLENNYTALQNAKYEGWYMAFTRKGRPRKG
                                                                                                                                                                                             ETEFYLCMNRKGKLVGKPDGTSKECVEIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKG
                                                                                                                                                                                                                                           RDDVSRKQLRLYQLYSRTSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGK 102
                                                                                                                                                                                                                                                               MGSPRSALSCLLLHLLVLCLQAQEGPGRGPALGRELASLFRAGREPQGVSQQHVREQSLV
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U36223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U47009; AAC50782.1; U47010; AAC50782.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U47010; AAC50782.1; J
AB014615; BAA28605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U36225;
                                                                                                                                                                                                                                                                                                            Similarity
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155
24
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AAC50782.
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AAB17893.1;
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                                                                                                  STANDARD;
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155
51
       Rodentia;
              Chordata;
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53.1%;
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JOINED.
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                                                                                                                                                                                                                                                                                                            Score 566; DB 1
Pred. No. 4e-46;
                                                                                                                                                                                                                                                                                                                                               ANDROGEN-INDUCED GROWTH FACTOR.

N-LINKED (GLCNAC...) (POTENTIA.
EGPGRGPALGRELASLFRAGREPQGYSQ ->
T (IN ISOFORM FGF-8B).

MISSING (IN ISOFORM FGF-8A).
Q -> QUTYQSSPNETQ (IN ISOFORM FG
     Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                        4C1EAF932A3A211D CRC64;
                                                                                                                                                                                                                                                                                                                                               -> QVTVQSSPNFTQ (IN ISOFORM FGF-8F).
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                209
                                                                                                                                                                   191
                                                                                                  268
                                                    (AIGF)
                                                                                                  A
                                                                                                                                                                                                                                                                                                                    ۳.
       Muridae;
                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                    Length 233
                                                    (HBGF-8)
                                                                                                                                                                                                                                                                                                    Indels
       Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                    (Fibroblast
                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                           VTVQSSENF
       Mus
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                       162
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STEET TETT WARRAND DRAW BERKER BERKER
Qy
                                                 Matches
                                                                    Query Match
Best Local
                                                                                                                                      VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                     Growth
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahmood R., Bresnick J., Hornbruch A., Mahony C., Morton N., Colquhoun K., Martin P., Lumsden A., Dickson C., Mason I.; "A role for FGF-8 in the initiation and maintenance of vertebrate
                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:99604; Fgf8.
InterPro: IPR002209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        limb bud outgrowth.";
Curr. Biol. 5:797-806(1995).
-I- FUNCTION: STIMULATES GROWTH OF THE CELLS IN AN AUTOCRINE MANNER.
MEDIATES HORMONAL ACTION ON THE GROWTH OF CANCER CELLS. COODERAN
WITH WNT-1 IN MOUSE MANMARY TUMOR VIRUS-INDUCED MURINE MANMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96082880; PubMed=7583127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macarthur C.A., Shankar D.B., Shackleford G.M.; "Fgf-8, activated by proviral insertion, cooperates with the Wnt-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Breast carcinoma;
MEDLINE=95191029; PubMed=7884899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumoto K.;
"Cloning and characterization of an androgen-induced essential for the androgen-dependent growth of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=93028380; PubMed=1409588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 89:8928-8932(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanaka A., Miyamoto
    _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMORIGENESIS.

ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; FGF-8C (SHOWN HERE), FGF-8B AND FGF-8A; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ABSENT IN NORMAL MAMMARY GLANDS AND DETECTED ONLY IN ADULT TESTIS AND OVARY AND IN MIDGESTATIONAL EMBRYOS. INDUCTION: BY ANDROGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
  MYSAPSACTCLCLHFLLLCFQVQVLVA-
                                                                                                                                                                                                                                                                                                                                                                                                                             PF00167; FGF; 1.
m; PD000831; HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D12483; BAA02051.1; -. D12482; BAA02050.1; -. U18673; AAA65387.1; -. Z48746; CAA88637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P31371; 1G82
                                                                                                                                                                                                                                                                                                                                                                                                                  SM00442; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                          PS00247; HBGF_FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit
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69:2501-2507(1995).
                                                                                                                             24
268
                                               Conservative
                                                                                                                                                                                                                              1
23
23
60
190
24
                                                                                                                                                                                                                           ; Mitogen; ; 1 22 23 268 23 268 23 23 60 60 60 90 190 24 87
                                                                                                                                      AA;
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30419
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                                                                  50.5%;
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                                                                                                                                                                                                                                                                                                                                                              Alternative splicing; Signal
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                                                                                                                                      W.
                                        Pred. No. 5.86
1; Mismatches
                                                                                                                                                                                                                         ANDROGEN-INDUCED GROWTH FACTOR.

PYRROLLDONE CARBOXYLIC ACID (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

VRSAAQKRGPGAGNPADTLGQGHEDRPFGQRSRAGKNFTNP
                                                                  Score 554.5;
Pred. No. 5.1
                                                                                                                                                  APNYPEEGSKEQRDSVLPKVTQR -> VTVQSSPNFTQ (IN ISOFORM FGF-8B).
MISSING (IN ISOFORM FGF-8A).
                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                      3330A9F342AD7109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                    8e-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
                                                                                       DB
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                                            46;
                                                                                       <u>ب</u>
                                                                                                                                      CRC64;
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EENVDF --
                                          Indels
                                                                                  Length
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' N.'
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                                                                                       268;
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                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
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                                          Gaps
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EMBL;
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Purification and characterization of a newly identified growth factor specific for epithelial cells."; force, Natl. Acad. Sci. U.S. A. 86:802-806(1989).

-I- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFER.

-I- SUBCELLULAR LOCATION: Secreted.

-I- TISSUE SPECIFICITY: EPITHELIAL CELL.

-I- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FIRST SIMILARITY SIMILA
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MEDLINE=89128865; PubMed=2915979;

MEDLINE=89128865; PubMed=8915979;

MEDLINE=8915979;

ME
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Aaronson S.A., Bottaro D.P., Miki T., Ron D., Finch P.W.,
Fleming T.P., Ahn J., Taylor W.G., Rubin J.S.;
"Keratinocyte growth factor. A fibroblast growth factor family
with unusual target cell specificity.";
Ann. N.Y. Acad. Sci. 638:62-77(1991).
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P21781;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE MEDLINE-89368897; Pubmed-2475908; Finch P.W., Rubin J.S., Miki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGF7
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15-JUN-2002 (Rel. 41, Last annotation update)
Keratinocyte growth factor precursor (KGF) (Fibroblast
7) (FGF-7) (HBGF-7).
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    M60828;
S81661;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB/N;
JOHES M.L., Dato M.E., Greenberg J.M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFIF -i- SUBCELLULAR LOCATION: Secreted.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The statement is no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                          Mason I.J., Fuller-Pace F., Smith R., Dickson C.; "FGF-7 (keratinocyte growth factor) expression during mouse development suggests roles in myogenesis, forebrain regional and epithelial-mesenchymal interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94242659; PubMed=8186145;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
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Pfam; PF00167; FGF;
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PIR; A36301;
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                                                                                           SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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; 22509 MW;
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30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 194;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                      EPITHELIAL CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; L
3.2e-11;
nes 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 194;
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RESULT FGF7/SH
ID 7-SH
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                        Mitchell J.E.A., McInnes C.J.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE
MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.
-i- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                         EMBL; Z46236; CAA86306.1;
HSSP; P31371; 1G82.
InterPro; IPR002209; HB/F.
InterPro; IPR002348; ILL_I
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).

Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P48808;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seguence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Keratinocyte growth factor precursor (KGF) (Fibroblast growth factor-7) (FGF-7) (HBGF-7).
FGF7 OR FGF-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGF7_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor; Mitogen; Signal SIGNAL 1 31 B
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ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
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EMBL; U58503; AAB01343.1;
PIR; S33227; S33227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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MGD; MGI:95521; Fgf7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -WYVGFTKKGRPRKGPKTRENQQDVHFM 175
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22347 MW;
                                                                                                                                                                                                                                            rmatics Institute. There are no restinstitutions as long as its content
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Pred. No. 4e-11;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KERATINOCYTE GROWTH FACTOR N-LINKED (GLCNAC. . .) (PO: 805C30D4B1D27C73 CRC64;
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                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                   Usage by
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                                                                                                                                                                                                                                                                                                                                                                                                                            Canatan H., Chang W.Y., Sugimoto Y., Shidaifat F., Kulp S.K., Brueggemeier R.W., Lin Y.C.;
"Keratinocyte growth factor (KGF/FGF-7) has a paracrine role prostate: molecular cloning of mRNA encoding canine KGF.";
DNA Cell Biol. 15:247-254(1996).
-1- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE MAJOR BARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGF7_CANFA STANDARD; PRT; 1
F79150;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANFA
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SEQUENCE
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                 InterPro; IPR002209; HB/F_growthfact
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=96226403; PubMed=8634153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor; Mitogen; Signal.

31 BY SIMILARITY.
                              PRINTS;
                                                                                                                                                     EMBL; U80800; AAB38972.1;
                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keratinocyte growth factor precursor (KGF) (Fibroblast growth factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00247; HBGF_FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKTAHFL 189
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                                                                                                                                P31371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
58; Conserv
PD000831; HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics
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22448 MW;
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80FAF4BC5B76F668 CRC64;
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SEQUENCE
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      "Interpreting a sequenced genome: Genome Res. 7:974-985(1997).
-!- FUNCTION: Required for larval
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the company of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                            Janke D.L., Schein J.E., Ha T., Franz N.W. Stewart H.I., Kuervers L.M., Baillie D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97474792; PubMed=9331368;
Janke D.L., Schein J.E., Ha T., Franz N.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; . Rhabditidae; Peloderinae; Caenorhabditis.
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LET-756 OR C05D11.4.
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Pred. No. 4.9e-11;
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; 8B4E56304B8F14D6 CRC64
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toward a cosmid transgenic.
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                                                                                              There are no restrictions on ong as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vatcher G.P.,
                                                                                                                                                                    EMBL
                                                                                                                                                                    a collaboration
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                                                                                                                                                                                                                                                                                                                                                                       rGF7_PIG STANDARD; PKI; 134 ALL.
Q9N198;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratinocyte growth factor precursor (KGF)
7)_[FGF-7] (HBGF-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _PIG
           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     Biol. Reprod. 62:1772-1778(2000)
-!- FUNCTION: GROWTH FACTOR ACTI
PARACRINE EFFECTOR OF NORMAL
                                                                                                                                                                                                                        MEDLINE=20297022; PubMed=10819782;
Ka H., Spencer T.E., Johnson G.A., Bazer F.W.;
Keratinocyte growth factor: expression by end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; C05D11.4; CE24786.
InterPro; IPR002209; HB/F_growthfact.
Pfam; PF00167; FGF; 1.
                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                    TISSUE-Endometrium;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).

    -!- SUBCELLULAR LOCATION: Secreted (By similarity).
    -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

                                                                                                                                                                                                               the porcine uterus
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00048; AAB53825.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ010553; CAA09234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 VTDLVVASLFHQPPSHPLFRQQTVTK-----PPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 RDDVSRKQL------RLYQLYSRTSGKHIQVL-----GRRISARG--ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSKFS--IVEFVSVAMSLVSIRGVETKNFICMDPSGKLYATPSSNYSTECVFLEEMMENY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDKYAQLLVE-TDTFGSQVRIKGKETEFYLCMNRKGKLVGKPDGT-SKECVFIEKVLENN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVDRIRKQLQDEEENGYPPADDRRRGALFCR-SGTWLEMLPIENPDDGSTRVKVHGTKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTALMSAKY----SGWYVGFTKKGRPRKGPKTRENQQDVHFM-----KRYPKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNLYASCAYGDRFNPWYIELRRSGKPRRGPNSKKRRKASHFLVVHHDLDRLRSPVPNGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00442; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD000831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00247; HBGF_FGF; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPELQKPFKYTTVTKRSRRIRPTHP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49569 MW;
                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.3%;
28.2%;
                                                                                                                                                                      NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                   precursor (KGF) (Fibroblast growth factor-
                                                                                                                                                                  ACTIVE ON KERATINOCYTES. POSSIBLE I ORMAL EPITHELIAL CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 190; DB 1;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-HIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255
                                                                                                                                                                                                                           endometrial epithelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                             Sus
                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                     POSSIBLE MAJOR
LIFERATION (BY
                                                                                   EMBL
                                                                                   a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 15
FGF7_RAT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          /) (FGF-7)
FGF7 OP
                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGF7_RAT
Q02195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS0024/; Mitogen; Signal Growth factor; Mitogen; Signal 31
                                                                                                                                                                                                                              factor type 7).";
In vitro Cell. Dev. Biol. 27A:437-438(1991).
In vitro Cell. Dev. Biol. 27A:437-438(1991).
In vitro Cell. Dev. Biol. 27A:437-438(1991).
In vitro Cell. Prosible
In vitro Cell. Proliferation.
MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
7) (FGF-7) (HBGF-7).
FGF7 OR FGF-7 OR KGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF217463; AAF26734.1; -.
HSSP; P31371; 1682.
InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
                                                                               EMBL; X56551; CAA39892.1; HSSP; P31371; 1G82.
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                  Yan G., Nikolaropoulos S., Wang F., McKeehan "Sequence of rat keratinocyte growth factor
                                                                                                                                                                                                                                                                                                                 MEDLINE=91331931; PubMed=1869483;
Yan G., Nikolaropoulos S., Wang F., McKeehan W.L.;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00167; FGF; 1
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 SKECVFIEKVLENNYTALMSAK--YSG--WYVGFTKKGRPRKGPKTRENQQDVHFM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDCNFKELILENHYNTYASAKWTHSGGEMFVALNQKGVPVRGKKTKKEQKTAHFL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFHITCLVGTLSLDCNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRT--QW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPRIGKRGKVKGTQEMKNNYNIMEIRTVAVGI-VAIKGVVSEYYLAMNKEGKLYAKKE-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQVLGRRISARG--EDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKPDGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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22463 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.2%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KERATINOCYTE GROWTH FACTOR N-LINKED (GLCNAC. . .) (PO; BA449B5B45A731B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188.5; DB 1
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                             There are no restrictions ong as its content is in
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                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                   and
                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194;
                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                   for
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InterPro; IPR002209; HB/F\_growthfact.
InterPro; IPR002348; IL1\_HBGF.
Pfam; PF00167; FGF; 1.

SMART; SM00442; FGF; PRINTS; PR00262; IL1HBGF ProDom; PD000831; HB/F\_gı

HB/F\_growthfact;